



SEQUENCE LISTING

<110> DAI, KEN SHUO

<120> HUMAN ARL-RELATED GENE VARIANTS ASSOCIATED WITH CANCER

<130> U014798-3

<140> 10/653,681

<141> 2003-09-02

<160> 4

<170> PatentIn version 3.2

<210> 1

<211> 1090

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> VARIANT OF HUMAN ALDOSE REDUCTASE-LIKE GENE

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<221> CDS

<222> (70)..(333)

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Met Ala Thr Phe Val Glu Leu Ser Thr Lys Ala Lys Met Pro
1 5 10att gtg ggc ctg ggc act tgg aag tct cct ctc ggc aaa gtg aaa gaa 159
Ile Val Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu
15 20 25 30gca gtg aag gtg gcc att gat gca gga tat cgg cac att gac tgt gcc 207
Ala Val Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala
35 40 45tat gtc tat cag aat gaa cat gaa gtg ggg gaa gcc atc caa gag aag 255
Tyr Val Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys
50 55 60atc caa gag aag gct gtg aag cgg gag gac ctg ttc atc gtc agc aag 303
Ile Gln Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys
65 70 75ttg tgg ccc act tcc aga tcg aga agc tct tgaacaaaacc tggactgaaa 353
Leu Trp Pro Thr Ser Arg Ser Arg Ser Ser
80 85

tataaaccag tgactaacca ggttgagtgt cacccatacc tcacgcagga gaaactgatc 413

cagtactgcc actccaaggg catcaccgtt acggcctaca gccccctggg ctctccggat 473

agaccttggg ccaagccaga agacccttcc ctgctggagg atcccaagat taaggagatt 533

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 gcctgtaacg tgttgcaatc ctctcatttg gaagactatc ccttcgatgc agaattattga 773
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Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu Ala Val
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Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala Tyr Val
 35 40 45

Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys Ile Gln
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Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys Leu Trp
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Pro Thr Ser Arg Ser Arg Ser Ser
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<220>

<221> CDS

<222> (70)..(804)

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Met Ala Thr Phe Val Glu Leu Ser Thr Lys Ala Lys Met Pro
1 5 10

att gtg ggc ctg ggc act tgg aag tct cct ctc ggc aaa gtg aaa gaa 159
Ile Val Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu
15 20 25 30

gca gtg aag gtg gcc att gat gca gga tat cgg cac att gac tgt gcc 207
Ala Val Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala
35 40 45

tat gtc tat cag aat gaa cat gaa gtg ggg gaa gcc atc caa gag aag 255
Tyr Val Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys
50 55 60

atc caa gag aag gct gtg aag cgg gag gac ctg ttc atc gtc agc aag 303
Ile Gln Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys
65 70 75

ttg tgg ccc act ttc ttt gag aga ccc ctt gtg agg aaa gcc ttt gag 351
Leu Trp Pro Thr Phe Phe Glu Arg Pro Leu Val Arg Lys Ala Phe Glu
80 85 90

aag acc ctc aag gac ctg aag ctg agc tat ctg gac gtc tat ctt att 399
Lys Thr Leu Lys Asp Leu Lys Leu Ser Tyr Leu Asp Val Tyr Leu Ile
95 100 105 110

cac tgg cca cag gga ttc aag tct ggg gat gac ctt ttc ccc aaa gat 447
His Trp Pro Gln Gly Phe Lys Ser Gly Asp Leu Phe Pro Lys Asp
115 120 125

gat aaa ggt aat gcc atc ggt gga aaa gca acg ttc ttg gat gcc tgg 495
Asp Lys Gly Asn Ala Ile Gly Gly Lys Ala Thr Phe Leu Asp Ala Trp
130 135 140

gag gcc atg gag gag ctg gtg gat gag ggg ctg gtg aaa gcc ctt ggg 543
Glu Ala Met Glu Glu Leu Val Asp Glu Gly Leu Val Lys Ala Leu Gly
145 150 155

gtc tcc aat ttc agc cac ttc cag atc gag aag ctc ttg aac aaa cct 591
Val Ser Asn Phe Ser His Phe Gln Ile Glu Lys Leu Leu Asn Lys Pro
160 165 170

gga ctg aaa tat aaa cca gtg act aac cag gtt gag tgt cac cca tac 639
Gly Leu Lys Tyr Lys Pro Val Thr Asn Gln Val Glu Cys His Pro Tyr
175 180 185 190

ctc acg cag gag aaa ctg atc cag tac tgc cac tcc aag ggc atc acc	687
Leu Thr Gln Glu Lys Leu Ile Gln Tyr Cys His Ser Lys Gly Ile Thr	
195 200 205	
ggt acg gcc tac agc ccc ctg ggc tct ccg gat aga cct tgg gcc aag	735
Val Thr Ala Tyr Ser Pro Leu Gly Ser Pro Asp Arg Pro Trp Ala Lys	
210 215 220	
cca gaa gac cct tcc ctg ctg gag gat ccc aag att aag gag att gct	783
Pro Glu Asp Pro Ser Leu Leu Glu Asp Pro Lys Ile Lys Glu Ile Ala	
225 230 235	
gca aag cac tcc cca agt ctg tgacaccagc acgcattggt gagaacattc	834
Ala Lys His Ser Pro Ser Leu	
240 245	
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<220>
 <223> PEPTIDE ENCODED BY VARIANT OF HUMAN ALDOSE REDUCTASE-LIKE GENE

<400> 4

Met Ala Thr Phe Val Glu Leu Ser Thr Lys Ala Lys Met Pro Ile Val
1 5 10 15

Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu Ala Val
20 25 30

Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala Tyr Val
35 40 45

Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys Ile Gln
50 55 60

Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys Leu Trp

65		70		75		80
Pro Thr Phe Phe	Glu 85	Arg Pro Leu Val	Arg 90	Lys Ala Phe Glu	Lys 95	Thr
Leu Lys Asp	Leu 100	Lys Leu Ser Tyr	Leu 105	Asp Val Tyr Leu	Ile 110	His Trp
Pro Gln Gly	Phe 115	Lys Ser Gly	Asp 120	Asp Leu Phe Pro	Lys 125	Asp Asp Lys
Gly Asn Ala	Ile 130	Gly Gly Lys	Ala 135	Thr Phe Leu	Asp 140	Ala Trp Glu Ala
Met Glu Glu	Leu 145	Val Asp 150	Glu Gly Leu	Val Lys 155	Ala Leu Gly	Val Ser 160
Asn Phe Ser	His 165	Phe Gln Ile	Glu Lys 170	Leu Leu Asn	Lys 175	Pro Gly Leu
Lys Tyr Lys	Pro 180	Val Thr Asn	Gln Val 185	Glu Cys His	Pro 190	Tyr Leu Thr
Gln Glu Lys	Leu 195	Ile Gln Tyr	Cys 200	His Ser Lys	Gly 205	Ile Thr Val Thr
Ala Tyr Ser	Pro 210	Leu Gly Ser	Pro 215	Asp Arg Pro	Trp 220	Ala Lys Pro Glu
Asp Pro Ser	Leu 225	Leu Glu 230	Asp Pro Lys	Ile Lys 235	Glu Ile Ala	Ala Lys 240
His Ser Pro	Ser 245	Leu				